

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

5

(i) APPLICANT: Gruys, Kenneth J.

Mitsky, Timothy A.

Kishore, Ganesh M.

Slater, Steven C.

10

Padgett, Stephen R.

Stark, David M.

Hinchee, Maud A. W.

Clemente, Thomas E.

Connor-Ward, Dannette V.

15

Fedele, Mary J.

Fry, Joyce E.

Howe, Arlene R.

Rozman, Renee J.

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(ii) TITLE OF INVENTION: Methods of Optimizing Substrate Pools and  
Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyvalerate  
in Bacteria and Plants

(iii) NUMBER OF SEQUENCES: 11

25

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Gary M. Bond, Monsanto Company, A3SB

(B) STREET: 800 North Lindbergh Boulevard

(C) CITY: St. Louis

30

(D) STATE: Missouri

(E) COUNTRY: USA

(F) ZIP: 63167

(v) COMPUTER READABLE FORM:

35

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

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(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
5 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE: 13-MAR-1996  
10

(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Bond, Gary  
(B) REGISTRATION NUMBER: 29,283  
(C) REFERENCE/DOCKET NUMBER: 38-21(13585)A  
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(ix) TELECOMMUNICATION INFORMATION:  
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20

(2) INFORMATION FOR SEQ ID NO:1:  
  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1545 base pairs  
25 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)  
30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
35

ATGGCTGACT CGCAACCCCT GTCCGGTGCT CCGGAAGGTG CCGAATATTT AAGAGCAGTG 60

CTGCGCGCGC CGGTTTACGA GCGGCGCAG GTTACGCCGC TACAAAAAAT GGAAAAACTG 120

|    |  |      |
|----|--|------|
|    | TCGTCGCGTC TTGATAACGT CATTCTGGTG AAGCGCGAAG ATCGCCAGCC AGTGACACAGC | 180  |
|    | TTTAAGCTGC GCGGCGCATA CGCCATGATG GCGGGCCTGA CGGAAGAACA GAAAGCGCAC  | 240  |
| 5  | GGCGTGATCA CTGCTTCTGC GGGTAACCAC GCGCAGGGCG TCGCGTTTTTCTTCTGCGCGG  | 300  |
|    | TTAGGCGTGA AGGCCCTGAT CGTTATGCCA ACCGCCACCG CCGACATCAA AGTCGACCGG  | 360  |
| 10 | CTGCGCGGCT TCGGCGGCGA AGTGCTGCTC CACGCGCGCA ACTTTGATGA AGCGAAACGC  | 420  |
|    | AAAGCGATCG AACTGTCACA GCAGCAGGGG TTCACCTGGG TGCCGCCGTT CGACCATCCG  | 480  |
|    | ATGGTGATTG CCGGGCAAGG CACGCTGGCG CTGGAAGTGC TCCAGCAGGA CGCCCATCTC  | 540  |
| 15 | GACCGCGTAT TTGTGCCAGT CGGCGGCGGC GGTCTGGCTG CTTGCGTGGC GGTGCTGATC  | 600  |
|    | AAACAACTGA TGCCGCAAAT CAAAGTGATC GCCGTAGAAG CGGAAGACTC CGCCTGCCTG  | 660  |
| 20 | AAAGCAGCGC TGGATGCGGG TCATCCGGTT GATCTGCCGC GCGTAGGGCT ATTTGCTGAA  | 720  |
|    | GGCGTAGCGG TAAAACGCAT CGGTGACGAA ACCTTCCGTT TATGCCAGGA GTATCTCGAC  | 780  |
|    | GACATCATCA CCGTCGATAG CGATGCGATC TGTGCGGCGA TGAAGGATTT ATTCGAAGAT  | 840  |
| 25 | GTGCGCGCGG TGGCGGAACC CTCTGGCGCG CTGGCGCTGG CGGGAATGAA AAAATATATC  | 900  |
|    | GCCCTGCACA ACATTCGCGG CGAACGGCTG GCGCATATTC TTTCCGGTGC CAACGTGAAC  | 960  |
| 30 | TTCCACGGCC TGCGCTACGT CTCAGAACGC TGCGAACTGG TCGAACAGCG TGAAGCGTTG  | 1020 |
|    | TTGGCGGTGA CCATTCCGGA AGAAAAAGGC AGCTTCCTCA AATTCTGCCA ACTGCTTGGC  | 1080 |
|    | GGGCGTTCGG TCACCGAGTT CAACTACCGT TTTGCCGATG CCAAAAACGC CTGCATCTTT  | 1140 |
| 35 | GTCGGTGTGC GCCTGAGCCG CGGCCTCGAA GAGCGCAAAG AAATTTTGCA GATGCTCAAC  | 1200 |
|    | GACGGCGGCT ACAGCGTGGT TGATCTCTCC GACGACGAAA TGGCGAAGCT ACACGTGCGC  | 1260 |

TATATGGTCG GCGGACGTCC ATCGCATCCG TTGCAGGAAC GCCTCTACAG CTTCGAATTC 1320

CCGGAATCAC CGGGCGCGCT GCTGCGCTTC CTCAACACGC TGGGTACGTA CTGGAACATT 1380

5

TCTTTGTTCC ACTATCGCAG CCATGGCACC GACTACGGGC GCGTACTGGC GGCGTTCGAA 1440

CTTGCGCACC ATGAACCGGA TTTCGAAACC CGGCTGAATG AGCTGGGCTA CGATTGCCAC 1500

10 GACGAAACCA ATAACCCGGC GTTCAGGTTC TTTTGGCGG GTTAA 1545

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTTTTGGATC CGATATCTTA ACCCGCCAAA AAGAACCTGA ACGCCG 46

30 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid

35

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTGGATC CATGGCTGAC TCGCAACCCC TGTCGG

37

10 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 base pairs

(B) TYPE: nucleic acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

20 (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

25

CAGCTTCGAG TTCCCGGAAT CACCGGGCGC GTTCCTGCGC TTCC

44

(2) INFORMATION FOR SEQ ID NO:5:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1545 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5: .

5 ATGGCTGACT CGCAACCCCT GTCCGGTGCT CCGGAAGGTG CCGAATATTT AAGAGCAGTG 60  
 CTGCGCGCGC CGGTTTACGA GGCGGCGCAG GTTACGCCGC TACAAAAAAT GGAAAAACTG 120  
 TCGTCGCGTC TTGATAACGT CATTCTGGTG AAGCGCGAAG ATCGCCAGCC AGTGCACAGC 180  
 10 TTTAAGCTGC GCGGCGCATA CGCCATGATG GCGGGCCTGA CGGAAGAACA GAAAGCGCAC 240  
 GGCGTGATCA CTGCTTCTGC GGGTAACCAC GCGCAGGGCG TCGCGTTTTC TTCTGCGCGG 300  
 15 TTAGGCGTGA AGGCCCTGAT CGTTATGCCA ACCGCCACCG CCGACATCAA AGTCGACCGG 360  
 CTGCGCGGCT TCGGCGGCGA AGTGCTGCTC CACGGCGCGA ACTTTGATGA AGCGAAACGC 420  
 AAAGCGATCG AACTGTCACA GCAGCAGGGG TTCACCTGGG TGCCGCCGTT CGACCATCCG 480  
 20 ATGGTGATTG CCGGGCAAGG CACGCTGGCG CTGGAAGTGC TCCAGCAGGA CGCCCATCTC 540  
 GACCGCGTAT TTGTGCCAGT CGGCGGCGGC GGTCTGGCTG CTTGCGTGGC GGTGCTGATC 600  
 25 AAACAACTGA TGCCGCAAAT CAAAGTGATC GCCGTAGAAG CGGAAGACTC CGCCTGCCTG 660  
 AAAGCAGCGC TGGATGCGGG TCATCCGGTT GATCTGCCGC GCGTAGGGCT ATTTGCTGAA 720  
 GGCGTAGCGG TAAAACGCAT CGGTGACGAA ACCTTCCGTT TATGCCAGGA GTATCTCGAC 780  
 30 GACATCATCA CCGTCGATAG CGATGCGATC TGTGCGGCGA TGAAGGATTT ATTCGAAGAT 840  
 GTGCGCGCGG TGGCGGAACC CTCTGGCGCG CTGGCGCTGG CGGGAATGAA AAAATATATC 900  
 35 GCCCTGCACA ACATTGCGCG CGAACGGCTG GCGCATATTC TTCCGGTGTC CAACGTGAAC 960  
 TTCCACGGCC TGCCTACGT CTCAGAACGC TCGAACTGG TCGAACAGCG TGAAGCGTTG 1020

TTGGCGGTGA CCATTCCGGA AGAAAAAGGC AGCTTCCTCA AATTCTGCCA ACTGCTTGGC 1080

GGGCGTTTCG TCACCGAGTT CAACTACCGT TTTGCCGATG CAAAAACGC CTGCATCTTT 1140

5 GTCGGTGTGC GCCTGAGCCG CGGCCTCGAA GAGCGCAAAG AAATTTTGCA GATGCTCAAC 1200

GACGGCGGGCT ACAGCGTGGT TGATCTCTCC GACGACGAAA TGGCGAAGCT ACACGTGCGC 1260

TATATGGTCG GCGGACGTCC ATCGCATCCG TTGCAGGAAC GCCTCTACAG CTTCGAGTTC 1320

10 CCGGAATCAC CGGGCGCGTT CCTGCGCTTC CTCAACACGC TGGGTACGTA CTGGAACATT 1380

TCTTTGTTCC ACTATCGCAG CCATGGCACC GACTACGGGC GCGTACTGGC GCGGTTTCGAA 1440

15 CTTGGCGACC ATGAACCGGA TTTCGAAACC CGGCTGAATG AGCTGGGCTA CGATTGCCAC 1500

GACGAAACCA ATAACCCGGC GTTCAGGTTC TTTTGGCGG GTTAA 1545

(2) INFORMATION FOR SEQ ID NO:6:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

35 TATCGCAGCC ACGGCACCGA CTACGGGCGC GTACTGGCGG CGTTCGAATT TGGCGACCAT 60

GAACC 65

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1545 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

15

ATGGCTGACT CGCAACCCCT GTCCGGTGCT CCGGAAGGTG CCGAATATTT AAGAGCAGTG 60

CTGCGCGCGC CGGTTTACGA GCGGGCGCAG GTTACGCCGC TACAAAAAAT GGAAAAACTG 120

20

TCGTGCGGTC TTGATAACGT CATTCTGGTG AAGCGGAAG ATCGCCAGCC AGTGCACAGC 180

TTTAAGCTGC GCGGCGCATA CGCCATGATG GCGGGCCTGA CGGAAGAACA GAAAGCGCAC 240

GGCGTGATCA CTGCTTCTGC GGGTAACCAC GCGCAGGGCG TCGCGTTTTT TTCTGCGCGG 300

25

TTAGGCGTGA AGGCCCTGAT CGTTATGCCA ACCGCCACCG CCGACATCAA AGTCGACCGG 360

CTGCGCGGCT TCGGCGGCGA AGTGCTGCTC CACGGCGCGA ACTTTGATGA AGCGAAACGC 420

30

AAAGCGATCG AACTGTCACA GCAGCAGGGG TTCACCTGGG TGCCGCCGTT CGACCATCCG 480

ATGGTGATTG CCGGGCAAGG CACGCTGGCG CTGGAAGTGC TCCAGCAGGA CGCCCATCTC 540

GACCGCGTAT TTGTGCCAGT CGGCGGCGGC GGTCTGGCTG CTTGCGTGGC GGTGCTGATC 600

35

AAACAACTGA TGCCGCAAAT CAAAGTGATC GCCGTAGAAG CGGAAGACTC CGCCTGCCTG 660

AAAGCAGCGC TGGATGCGGG TCATCCGGTT GATCTGCCGC GCGTAGGGCT ATTTGCTGAA 720



GGCGTAGCGG TAAAACGCAT CGGTGACGAA ACCTTCCGTT TATGCCAGGA GTATCTCGAC 780  
GACATCATCA CCGTCGATAG CGATGCGATC TGTGCGGCGA TGAAGGATTT ATTCGAAGAT 840  
5 GTGCGCGCGG TGGCGGAACC CTCTGGCGCG CTGGCGCTGG CGGGAATGAA AAAATATATC 900  
GCCCTGCACA ACATTCGCGG CGAACGGCTG GCGCATATTC TTTCCGGTGC CAACGTGAAC 960  
10 TTCCACGGCC TGCCTACGT CTCAGAACGC TCGAACTGG TCGAACAGCG TGAAGCGTTG 1020  
TTGGCGGTGA CCATTCCGGA AGAAAAAGGC AGCTTCCTCA AATTCTGCCA ACTGCTTGGC 1080  
GGGCGTTCGG TCACCGAGTT CAACTACCGT TTTGCCGATG CCAAAAACGC CTGCATCTTT 1140  
15 GTCGGTGTGC GCCTGAGCCG CGGCCTCGAA GAGCGCAAAG AAATTTTGCA GATGCTCAAC 1200  
GACGGCGGCT ACAGCGTGGT TGATCTCTCC GACGACGAAA TGGCGAAGCT ACACGTGCGC 1260  
20 TATATGGTCG GCGGACGTCC ATCGCATCCG TTGCAGGAAC GCCTCTACAG CTTCGAATTC 1320  
CCGGAATCAC CGGGCGCGCT GCTGCGCTTC CTCAACACGC TGGGTACGTA CTGGAACATT 1380  
TCTTTGTTCC ACTATCGCAG CCACGGCACC GACTACGGGC GCGTACTGGC GGCCTTCGAA 1440  
25 TTTGGCGACC ATGAACCGGA TTTCGAAACC CGGCTGAATG AGCTGGGCTA CGATTGCCAC 1500  
GACGAAACCA ATAACCCGGC GTTCAGGTTT TTTTGGCGG GTTAA 1545

## 30 (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1545 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGGCTGACT CGCAACCCCT GTCCGGTGCT CCGGAAGGTG CCGAATATTT AAGAGCAGTG 60

CTGCGCGCGC CGGTTTACGA GGCGGCGCAG GTTACGCCGC TACAAAAAAT GGAAAACTG 120

10 TCGTCGCGTC TTGATAACGT CATTCTGGTG AAGCGCGAAG ATCGCCAGCC AGTGCACAGC 180

TTTAAGCTGC GCGGCGCATA CGCCATGATG GCGGGCCTGA CGGAAGAACA GAAAGCGCAC 240

15 GGCGTGATCA CTGCTTCTGC GGGTAACCAC GCGCAGGGCG TCGCGTTTTT TTCTGCGCGG 300

TTAGGCGTGA AGGCCCTGAT CGTTATGCCA ACCGCCACCG CCGACATCAA AGTCGACCGG 360

CTGCGCGGCT TCGGCGGCGA AGTGCTGCTC CACGGCGCGA ACTTTGATGA AGCGAAACGC 420

20 AAAGCGATCG AACTGTCACA GCAGCAGGGG TTCACCTGGG TGCCGCCGTT CGACCATCCG 480

ATGGTGATTG CCGGGCAAGG CACGCTGGCG CTGGAAGTGC TCCAGCAGGA CGCCCATCTC 540

25 GACCGCGTAT TTGTGCCAGT CGGCGGCGGC GGTCTGGCTG CTTGCGTGGC GGTGCTGATC 600

AAACAACTGA TGCCGCAAAT CAAAGTGATC GCCGTAGAAG CGGAAGACTC CGCCTGCCTG 660

AAAGCAGCGC TGGATGCGGG TCATCCGGTT GATCTGCCGC GCGTAGGGCT ATTTGCTGAA 720

30 GGCGTAGCGG TAAACGCAT CGGTGACGAA ACCTTCCGTT TATGCCAGGA GTATCTCGAC 780

GACATCATCA CCGTCGATAG CGATGCGATC TGTGCGGCGA TGAAGGATTT ATTCGAAGAT 840

35 GTGCGCGCGG TGGCGGAACC CTCTGGCGCG CTGGCGCTGG CGGGAATGAA AAAATATATC 900

GCCCTGCACA ACATTCGCGG CGAACGGCTG GCGCATATTC TTCCGGTGTC CAACGTGAAC 960

TTCCACGGCC TGCCTACGT CTCAGAACGC TCGAACTGG TCGAACAGCG TGAAGCGTTG 1020

TTGGCGGTGA CCATTCCGGA AGAAAAAGGC AGCTTCCTCA AATTCTGCCA ACTGCTTGGC 1080

5 GGGCGTTCGG TCACCGAGTT CAACTACCGT TTTGCCGATG CCAAAAACGC CTGCATCTTT 1140

GTCGGTGTGC GCCTGAGCCG CGGCCTCGAA GAGCGCAAAG AAATTTTGCA GATGCTCAAC 1200

GACGGCGGCT ACAGCGTGGT TGATCTCTCC GACGACGAAA TGGCGAAGCT ACACGTGCGC 1260

10 TATATGGTCG GCGGACGTCC ATCGCATCCG TTGCAGGAAC GCCTCTACAG CTTGAGTTC 1320

CCGAATCAC CGGGCGCGTT CCTGCGCTTC CTCAACACGC TGGGTACGTA CTGGAACATT 1380

15 TCTTTGTTCC ACTATCGCAG CCACGGCACC GACTACGGGC GCGTACTGGC GGC GTTCGAA 1440

TTTGGCGACC ATGAACCGGA TTTCGAAACC CGGCTGAATG AGCTGGGCTA CGATTGCCAC 1500

GACGAAACCA ATAACCCGGC GTTCAGGTTC TTTTGGCGG GTTAA 1545

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(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 1185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGACGCGTG AAGTGGTAGT GGTAAGCGGT GTCCGTACCG CGATCGGGAC CTTTGGCGGC 60

|    |   |      |
|----|---|------|
|    | AGCCTGAAGG ATGTGGCACC GCGGAGCTG GCGCACTGG TGGTGC GCGA GCGCTGGCG   | 120  |
|    | CGCGCGCAGG TGTCGGGCGA CGATGTCGGC CACGTGGTAT TCGGCAACGT GATCCAGACC | 180  |
| 5  | GAGCCGCGCG ACATGTATCT GGGCCGCGTC GCGGCCGTCA ACGGCGGGT GACGATCAAC  | 240  |
|    | GGCCCCGCGC TGACCGTGAA CCGCCTGTGC GGCTCGGGCC TGCAGGCCAT TGTCAGCGCC | 300  |
|    | GCGCAGACCA TCCTGCTGGG CGATACCGAC GTCGCCATCG GCGGCGGCGC GGAAAGCATG | 360  |
| 10 | AGCCGCGCAC CGTACCTGGC GCCGGCAGCG CGCTGGGGCG CACGCATGGG CGACGCCGGC | 420  |
|    | CTGGTCGACA TGATGCTGGG TCGCTGCAC GATCCCTTCC ATCGCATCCA CATGGGCGTG  | 480  |
| 15 | ACCGCCGAGA ATGTCGCCAA GGAATACGAC ATCTCGCGCG CGCAGCAGGA CGAGGCCGCG | 540  |
|    | CTGGAATCGC ACCGCCGCGC TTCGGCAGCG ATCAAGGCCG GCTACTTCAA GGACCAGATC | 600  |
|    | GTCCCGGTGG TGAGCAAGGG CCGCAAGGGC GACGTGACCT TCGACACCGA CGAGCACGTG | 660  |
| 20 | CGCCATGACG CCACCATCGA CGACATGACC AAGCTCAGGC CGGTCTTCGT CAAGGAAAAC | 720  |
|    | GGCACGGTCA CGGCCGGCAA TGCCTCGGGC CTGAACGACG CCGCCGCCGC GGTGGTGATG | 780  |
| 25 | ATGGAGCGCG CCGAAGCCGA GCGCCGCGGC CTGAAGCCGC TGGCCCGCCT GGTGTCGTAC | 840  |
|    | GGCCATGCCG GCGTGGACCC GAAGGCCATG GGCATCGGCC CGGTGCCGGC GACGAAGATC | 900  |
|    | GCGCTGGAGC GCGCCGGCCT GCAGGTGTCG GACCTGGACG TGATCGAAGC CAACGAAGCC | 960  |
| 30 | TTTGCCGCAC AGGCGTGCGC CGTGACCAAG GCGCTCGGTC TGGACCCGGC CAAGGTAAAC | 1020 |
|    | CCGAACGGCT CGGGCATCTC GCTGGGCCAC CCGATCGGCG CCACCGGTGC CCTGATCAGC | 1080 |
| 35 | GTGAAGGCGC TGCATGAGCT GAACCGCGTG CAGGGCCGCT ACGCGCTGGT GACGATGTGC | 1140 |
|    | ATCGGCGGCG GGCAGGGCAT TGCCGCCATC TTCGAGCGTA TCTGA                 | 1185 |

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## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

15

Thr Arg Glu Val Val Val Val Ser Gly Val Arg Thr Ala Ile Gly  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:11:

20

## (1) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 394 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

35 Met Thr Arg Glu Val Val Val Val Ser Gly Val Arg Thr Ala Ile Gly  
1 5 10 15

Thr Phe Gly Gly Ser Leu Lys Asp Val Ala Pro Ala Glu Leu Gly Ala  
20 25 30

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Leu Val Val Arg Glu Ala Leu Ala Arg Ala Gln Val Ser Gly Asp Asp  
 35 40 45

5 Val Gly His Val Val Phe Gly Asn Val Ile Gln Thr Glu Pro Arg Asp  
 50 55 60

Met Tyr Leu Gly Arg Val Ala Ala Val Asn Gly Gly Val Thr Ile Asn  
 65 70 75 80

10 Ala Pro Ala Leu Thr Val Asn Arg Leu Cys Gly Ser Gly Leu Gln Ala  
 85 90 95

Ile Val Ser Ala Ala Gln Thr Ile Leu Leu Gly Asp Thr Asp Val Ala  
 15 100 105 110

Ile Gly Gly Gly Ala Glu Ser Met Ser Arg Ala Pro Tyr Leu Ala Pro  
 115 120 125

20 Ala Ala Arg Trp Gly Ala Arg Met Gly Asp Ala Gly Leu Val Asp Met  
 130 135 140

Met Leu Gly Ala Leu His Asp Pro Phe His Arg Ile His Met Gly Val  
 145 150 155 160

25 Thr Ala Glu Asn Val Ala Lys Glu Tyr Asp Ile Ser Arg Ala Gln Gln  
 165 170 175

Asp Glu Ala Ala Leu Glu Ser His Arg Arg Ala Ser Ala Ala Ile Lys  
 30 180 185 190

Ala Gly Tyr Phe Lys Asp Gln Ile Val Pro Val Val Ser Lys Gly Arg  
 195 200 205

35 Lys Gly Asp Val Thr Phe Asp Thr Asp Glu His Val Arg His Asp Ala  
 210 215 220

Thr Ile Asp Asp Met Thr Lys Leu Arg Pro Val Phe Val Lys Glu Asn

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|    |   |     |     |     |
|----|---|-----|-----|-----|
|    | 225   | 230 | 235 | 240 |
|    | Gly Thr Val Thr Ala Gly Asn Ala Ser Gly Leu Asn Asp Ala Ala Ala |     |     |     |
|    |   | 245 | 250 | 255 |
| 5  | Ala Val Val Met Met Glu Arg Ala Glu Ala Glu Arg Arg Gly Leu Lys |     |     |     |
|    | 260   | 265 | 270 |     |
|    | Pro Leu Ala Arg Leu Val Ser Tyr Gly His Ala Gly Val Asp Pro Lys |     |     |     |
| 10 | 275   | 280 | 285 |     |
|    | Ala Met Gly Ile Gly Pro Val Pro Ala Thr Lys Ile Ala Leu Glu Arg |     |     |     |
|    | 290   | 295 | 300 |     |
| 15 | Ala Gly Leu Gln Val Ser Asp Leu Asp Val Ile Glu Ala Asn Glu Ala |     |     |     |
|    | 305   | 310 | 315 | 320 |
|    | Phe Ala Ala Gln Ala Cys Ala Val Thr Lys Ala Leu Gly Leu Asp Pro |     |     |     |
|    | 325   | 330 | 335 |     |
| 20 | Ala Lys Val Asn Pro Asn Gly Ser Gly Ile Ser Leu Gly His Pro Ile |     |     |     |
|    | 340   | 345 | 350 |     |
|    | Gly Ala Thr Gly Ala Leu Ile Thr Val Lys Ala Leu His Glu Leu Asn |     |     |     |
| 25 | 355   | 360 | 365 |     |
|    | Arg Val Gln Gly Arg Tyr Ala Leu Val Thr Met Cys Ile Gly Gly Gly |     |     |     |
|    | 370   | 375 | 380 |     |
| 30 | Gln Gly Ile Ala Ala Ile Phe Glu Arg Ile                         |     |     |     |
|    | 385   | 390 |     |     |

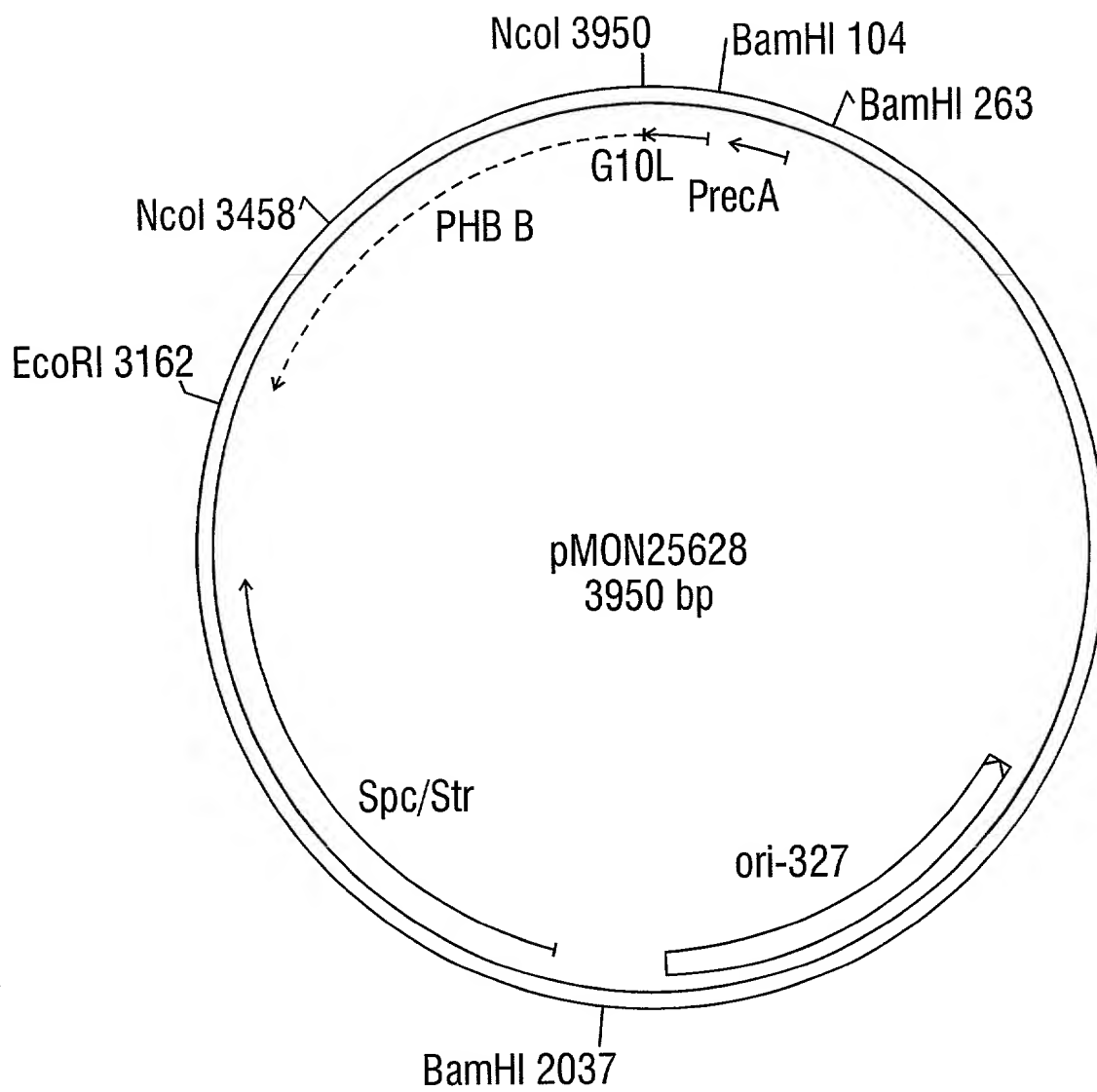


FIG. 18



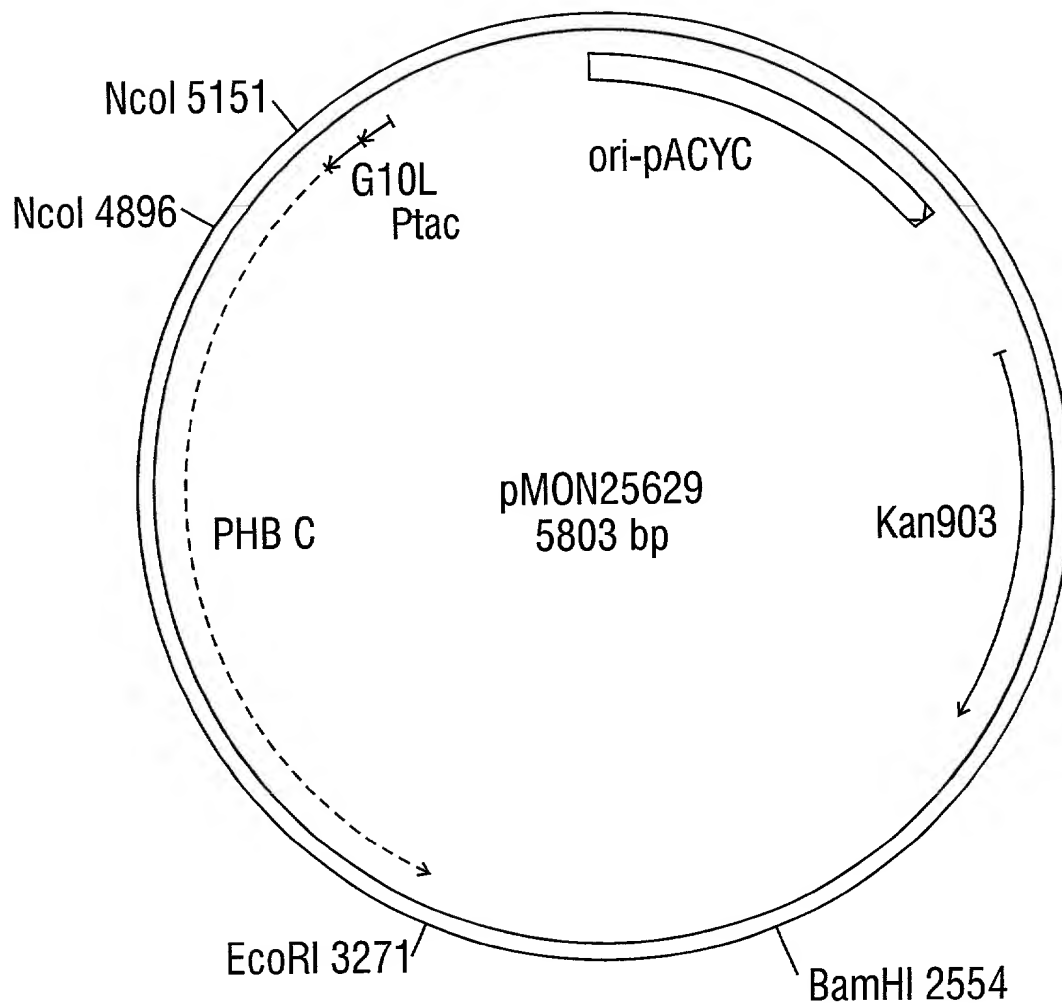


FIG. 19

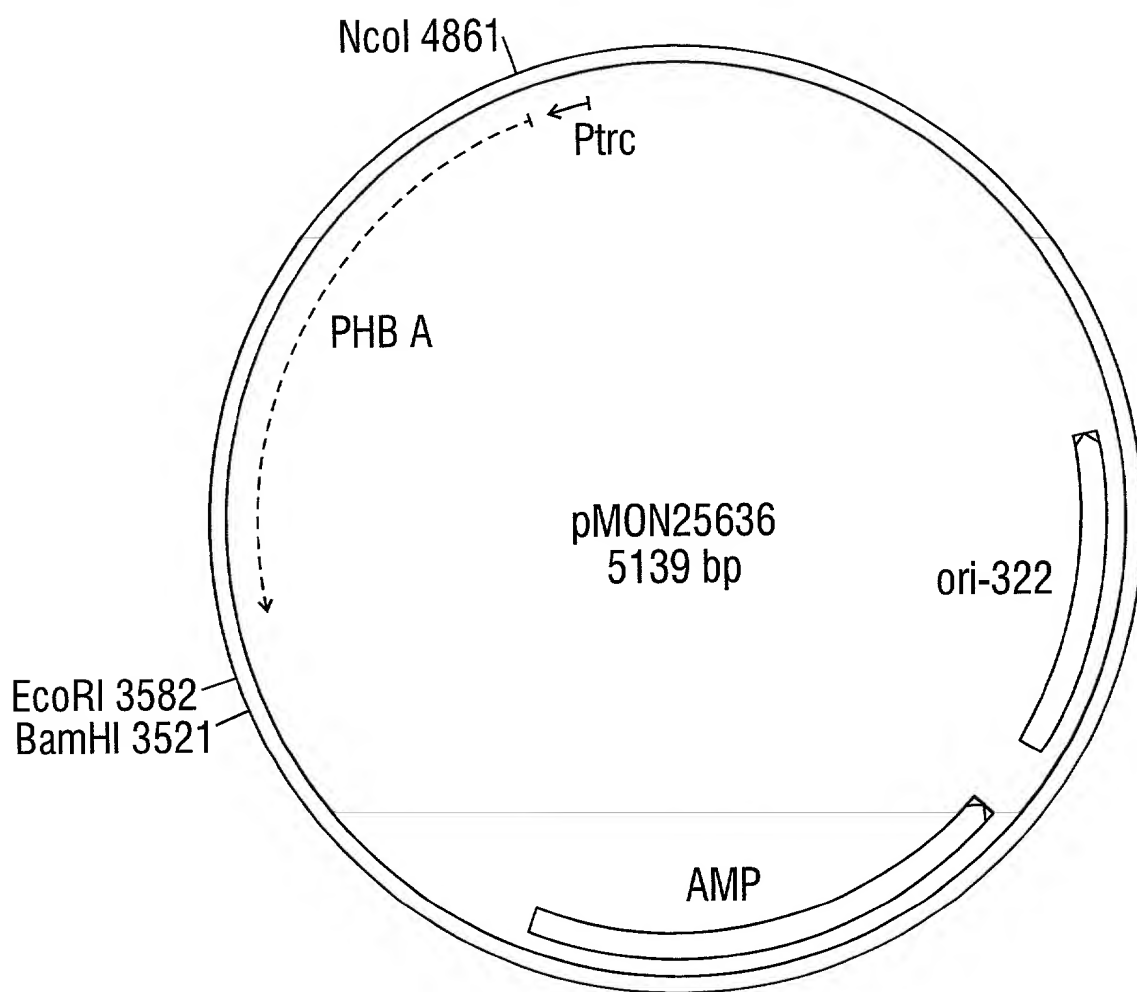


FIG. 20

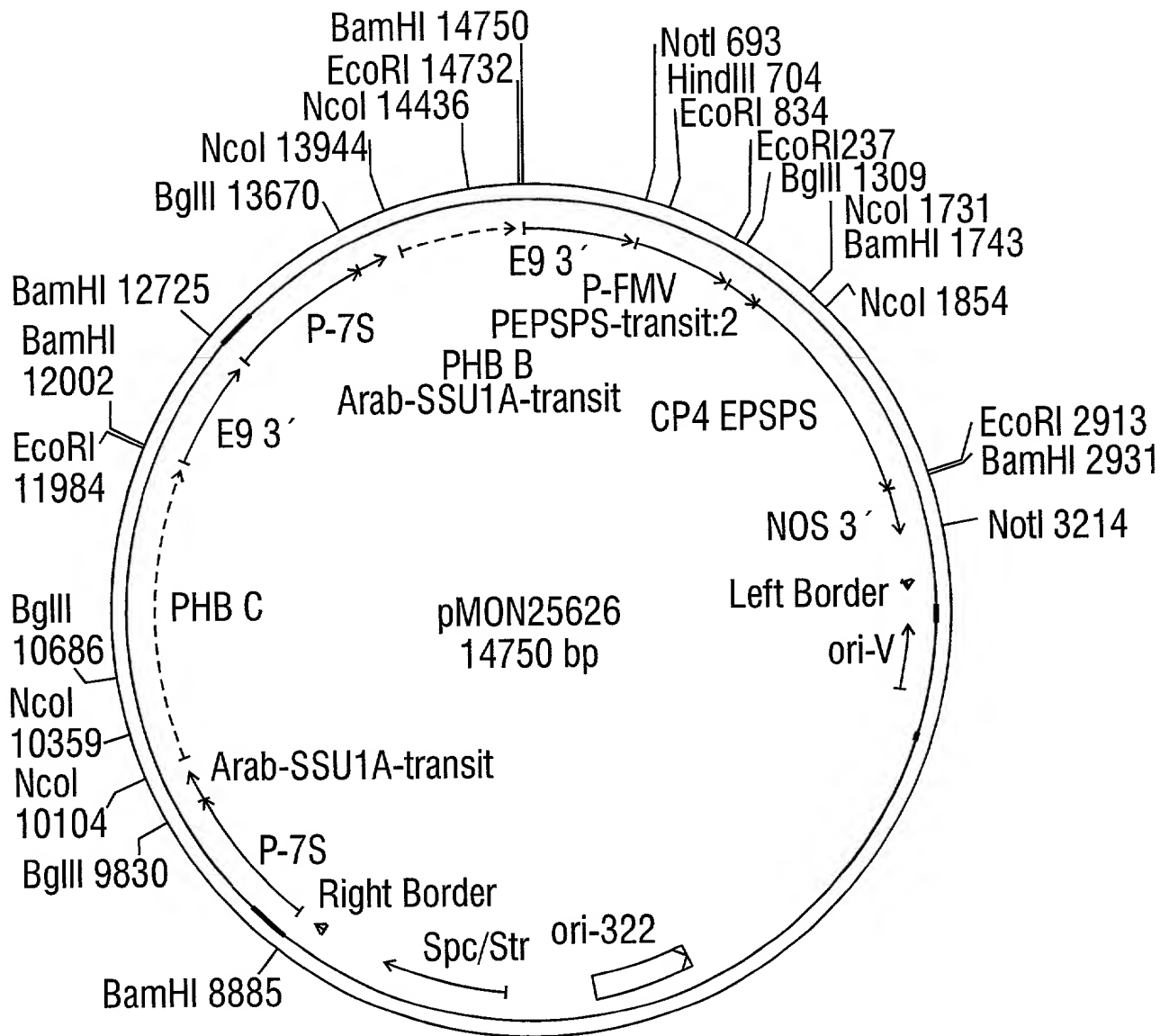


FIG. 21

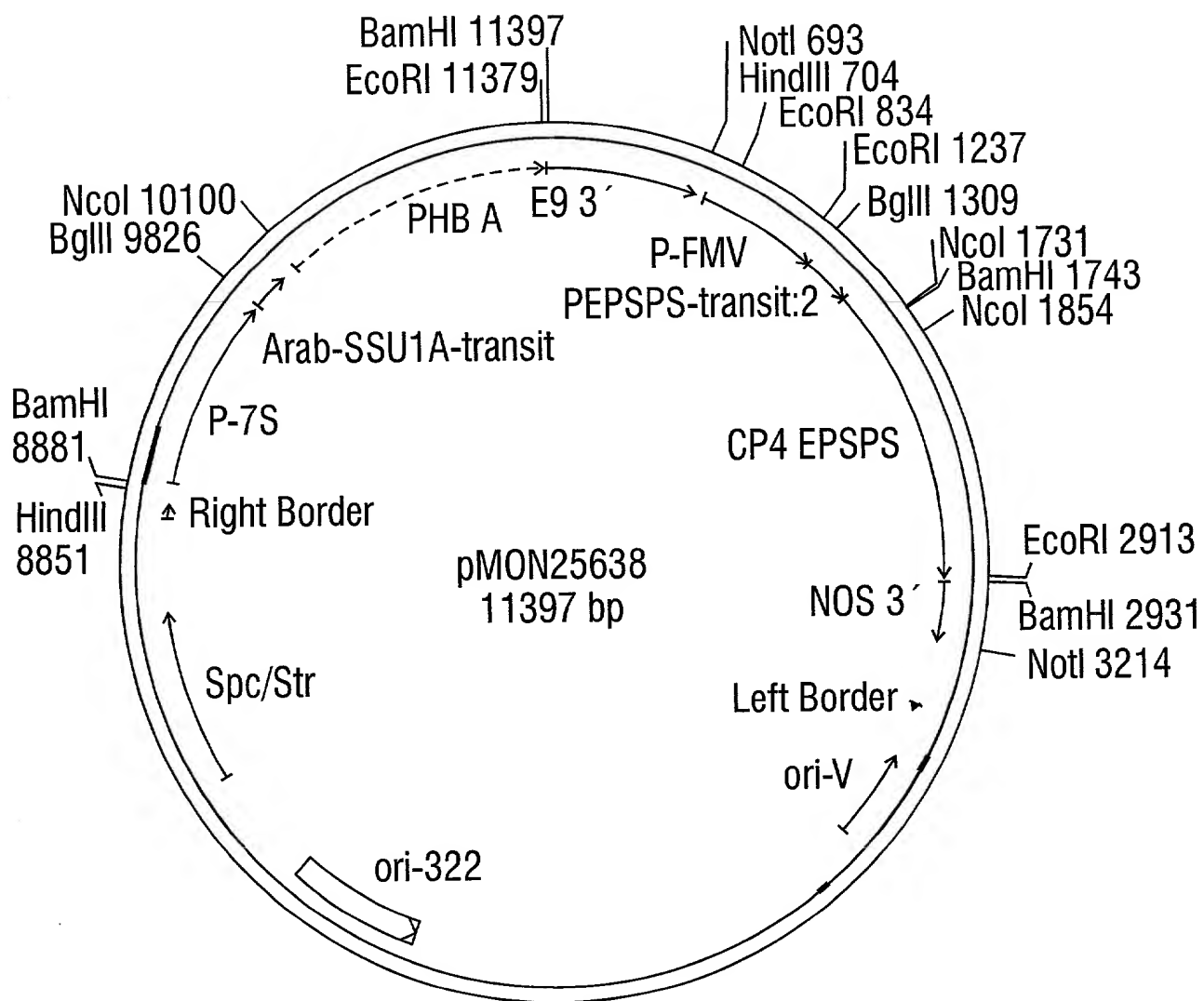


FIG. 22